

Patent Application US/07/800,364A

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S3925.raw

(1) GENERAL INFORMATION:

(i) APPLICANT: Hewick, Rodney M.
Wang, Jack H.
Wozney, John M.
Celeste, Anthony J.

(ii) TITLE OF INVENTION: Bone and Cartilage Inductive Proteins

(iii) NUMBER OF SEQUENCES: 14

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Legal Affairs, Genetics Institute, Inc.
(B) STREET: 87 CambridgePark Drive
(C) CITY: Cambridge
(D) STATE: MA
(E) COUNTRY: USA
(F) ZIP: 02140

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/800,364
(B) FILING DATE: 26-NOV-1991
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Kapinos, Ellen J.
(B) REGISTRATION NUMBER: 32,245
(C) REFERENCE/DOCKET NUMBER: GI 5182A

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 617-876-1170
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

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53 (iv) ANTI-SENSE: NO
54
55 (vi) ORIGINAL SOURCE:
56 (F) TISSUE TYPE: Bone
57
58
59 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
60
61 Arg His Glu Leu Tyr Val Ser Phe Gln Asp Leu Gly Trp Leu Asp Trp
62 1 5 10 15
63
64 Val Ile Ala Pro Gln Gly Tyr
65 20
66
67 (2) INFORMATION FOR SEQ ID NO:2:
68
69 (i) SEQUENCE CHARACTERISTICS:
70 (A) LENGTH: 18 amino acids
71 (B) TYPE: amino acid
72 (C) STRANDEDNESS: single
73 (D) TOPOLOGY: unknown
74
75 (ii) MOLECULE TYPE: peptide
76
77 (iii) HYPOTHETICAL: NO
78
79 (iv) ANTI-SENSE: NO
80
81 (v) FRAGMENT TYPE: internal
82
83 (vi) ORIGINAL SOURCE:
84 (A) ORGANISM: Bos taurus
85 (F) TISSUE TYPE: Bone
86
87
88 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
89
90 Leu Ser Ala Thr Ser Val Leu Tyr Tyr Asp Ser Ser Asn Asn Val Ile
91 1 5 10 15
92
93 Leu Arg
94
95
96 (2) INFORMATION FOR SEQ ID NO:3:
97
98 (i) SEQUENCE CHARACTERISTICS:
99 (A) LENGTH: 7 amino acids
100 (B) TYPE: amino acid
101 (C) STRANDEDNESS: single
102 (D) TOPOLOGY: unknown
103
104 (ii) MOLECULE TYPE: peptide

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105
106 (iii) HYPOTHETICAL: NO
107
108 (iv) ANTI-SENSE: NO
109
110 (vi) ORIGINAL SOURCE:
111 (A) ORGANISM: Bos taurus
112 (F) TISSUE TYPE: Bone
113
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115 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
116
117 Ala Cys Cys Ala Pro Thr Lys
118 1 5
119
120 (2) INFORMATION FOR SEQ ID NO:4:
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122 (i) SEQUENCE CHARACTERISTICS:
123 (A) LENGTH: 23 amino acids
124 (B) TYPE: amino acid
125 (C) STRANDEDNESS: single
126 (D) TOPOLOGY: unknown
127
128 (ii) MOLECULE TYPE: peptide
129
130 (iii) HYPOTHETICAL: NO
131
132 (vi) ORIGINAL SOURCE:
133 (A) ORGANISM: Bos taurus
134 (F) TISSUE TYPE: Bone
135
136
137 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
138
139 Thr Asn Glu Leu Pro Pro Pro Asn Lys Leu Pro Gly Ile Phe Asp Asp
140 1 5 10 15
141
142 Val His Gly Ser His Gly Arg
143 20
144
145 (2) INFORMATION FOR SEQ ID NO:5:
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147 (i) SEQUENCE CHARACTERISTICS:
148 (A) LENGTH: 80 base pairs
149 (B) TYPE: nucleic acid
150 (C) STRANDEDNESS: double
151 (D) TOPOLOGY: linear
152
153 (ii) MOLECULE TYPE: DNA (genomic)
154
155 (iii) HYPOTHETICAL: NO
156

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157 (iv) ANTI-SENSE: NO
158
159 (vi) ORIGINAL SOURCE:
160 (A) ORGANISM: Bos taurus
161
162 (vii) IMMEDIATE SOURCE:
163 (B) CLONE: acc30
164
165 (viii) POSITION IN GENOME:
166 (C) UNITS: bp
167
168 (ix) FEATURE:
169 (A) NAME/KEY: CDS
170 (B) LOCATION: 25..57
171
172
173 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
174
175 GGATCCGCGT GCTGTGCTCC GACC AAG CTG AGC GCC ACC TCC GTG CTC TAC 51
176 Lys Leu Ser Ala Thr Ser Val Leu Tyr
177 1 5
178
179 TAC GAC AGCAGCAACA ATGTAATTCT AGA 80
180 Tyr Asp
181 10
182
183
184 (2) INFORMATION FOR SEQ ID NO:6:
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186 (i) SEQUENCE CHARACTERISTICS:
187 (A) LENGTH: 11 amino acids
188 (B) TYPE: amino acid
189 (D) TOPOLOGY: linear
190
191 (ii) MOLECULE TYPE: protein
192
193 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
194
195 Lys Leu Ser Ala Thr Ser Val Leu Tyr Tyr Asp
196 1 5 10
197
198 (2) INFORMATION FOR SEQ ID NO:7:
199
200 (i) SEQUENCE CHARACTERISTICS:
201 (A) LENGTH: 199 base pairs
202 (B) TYPE: nucleic acid
203 (C) STRANDEDNESS: double
204 (D) TOPOLOGY: linear
205
206 (ii) MOLECULE TYPE: DNA (genomic)
207
208 (iii) HYPOTHETICAL: NO

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209
210 (vi) ORIGINAL SOURCE:
211 (A) ORGANISM: Bos Taurus
212
213 (vii) IMMEDIATE SOURCE:
214 (A) LIBRARY: Bovine genomic
215 (B) CLONE: Lambda 9800-10
216
217 (viii) POSITION IN GENOME:
218 (C) UNITS: bp
219
220 (ix) FEATURE:
221 (A) NAME/KEY: exon
222 (B) LOCATION: 30..199
223
224 (ix) FEATURE:
225 (A) NAME/KEY: intron
226 (B) LOCATION: 1..29
227
228 (ix) FEATURE:
229 (A) NAME/KEY: CDS
230 (B) LOCATION: 30..179
231
232
233 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
234
235 TGCCCGCTGC CCCCTCCCGC CCCC GCCAG GTG CAC CTG CTG AAG CCG CAC GCG 53
236 Val His Leu Leu Lys Pro His Ala
237 1 5
238
239 GTC CCC AAG GCG TGC TGC GCG CCC ACC AAG CTG AGC GCC ACT TCC GTG 101
240 Val Pro Lys Ala Cys Cys Ala Pro Thr Lys Leu Ser Ala Thr Ser Val
241 10 15 20
242
243 CTC TAC TAC GAC AGC AGC AAC AAC GTC ATC CTG CGC AAG CAC CGC AAC 149
244 Leu Tyr Tyr Asp Ser Ser Asn Asn Val Ile Leu Arg Lys His Arg Asn
245 25 30 35 40
246
247 ATG GTG GTC CGC GCC TGC GGC TGC CAC TGAGGCCCA ACTCCACCGG 196
248 Met Val Val Arg Ala Cys Gly Cys His
249 45 50
250
251 CAG 199
252
253
254 (2) INFORMATION FOR SEQ ID NO:8:
255
256 (i) SEQUENCE CHARACTERISTICS:
257 (A) LENGTH: 49 amino acids
258 (B) TYPE: amino acid
259 (D) TOPOLOGY: linear
260

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261 (ii) MOLECULE TYPE: protein
262
263 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
264
265 Val His Leu Leu Lys Pro His Ala Val Pro Lys Ala Cys Cys Ala Pro
266 1 5 10 15
267
268 Thr Lys Leu Ser Ala Thr Ser Val Leu Tyr Tyr Asp Ser Ser Asn Asn
269 20 25 30
270
271 Val Ile Leu Arg Lys His Arg Asn Met Val Val Arg Ala Cys Gly Cys
272 35 40 45
273
274 His
275
276
277
278 (2) INFORMATION FOR SEQ ID NO:9:
279
280 (i) SEQUENCE CHARACTERISTICS:
281 (A) LENGTH: 172 base pairs
282 (B) TYPE: nucleic acid
283 (C) STRANDEDNESS: double
284 (D) TOPOLOGY: linear
285
286 (ii) MOLECULE TYPE: DNA (genomic)
287
288 (iii) HYPOTHETICAL: NO
289
290 (vi) ORIGINAL SOURCE:
291 (A) ORGANISM: Bos taurus
292
293 (vii) IMMEDIATE SOURCE:
294 (A) LIBRARY: Bovine genomic
295 (B) CLONE: Lambda 9800-10
296
297 (viii) POSITION IN GENOME:
298 (C) UNITS: bp
299
300 (ix) FEATURE:
301 (A) NAME/KEY: exon
302 (B) LOCATION: 51..161
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304 (ix) FEATURE:
305 (A) NAME/KEY: intron
306 (B) LOCATION: 1..50
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308 (ix) FEATURE:
309 (A) NAME/KEY: intron
310 (B) LOCATION: 162..172
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312 (ix) FEATURE:

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313 (A) NAME/KEY: CDS
314 (B) LOCATION: 51..161
315
316
317 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
318
319 GGGGTGGGAG GGCACGTGGA TGGGACTCAC CTTCTCCCAC TACCCCCCAG GAC TGG 56
320 Asp Trp
321 1
322
323 GTC ATC GCC CCC CAA GGC TAC TCA GCC TAT TAC TGT GAA GGG GAG TGC 104
324 Val Ile Ala Pro Gln Gly Tyr Ser Ala Tyr Tyr Cys Glu Gly Glu Cys
325 5 10 15
326
327 TCC TTC CCG CTG GAC TCC TGC ATG AAC GCC ACC AAC CAC GCC ATC CTG 152
328 Ser Phe Pro Leu Asp Ser Cys Met Asn Ala Thr Asn His Ala Ile Leu
329 20 25 30
330
331 CAG TCC CTG GTCAGTACCT C 172
332 Gln Ser Leu
333 35
334
335
336 (2) INFORMATION FOR SEQ ID NO:10:
337
338 (i) SEQUENCE CHARACTERISTICS:
339 (A) LENGTH: 37 amino acids
340 (B) TYPE: amino acid
341 (D) TOPOLOGY: linear
342
343 (ii) MOLECULE TYPE: protein
344
345 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:
346
347 Asp Trp Val Ile Ala Pro Gln Gly Tyr Ser Ala Tyr Tyr Cys Glu Gly
348 1 5 10 15
349
350 Glu Cys Ser Phe Pro Leu Asp Ser Cys Met Asn Ala Thr Asn His Ala
351 20 25 30
352
353 Ile Leu Gln Ser Leu
354 35
355
356 (2) INFORMATION FOR SEQ ID NO:11:
357
358 (i) SEQUENCE CHARACTERISTICS:
359 (A) LENGTH: 119 base pairs
360 (B) TYPE: nucleic acid
361 (C) STRANDEDNESS: double
362 (D) TOPOLOGY: linear
363
364 (ii) MOLECULE TYPE: DNA (genomic)

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365
366 (iii) HYPOTHETICAL: NO
367
368 (vi) ORIGINAL SOURCE:
369 (A) ORGANISM: Bos taurus
370
371 (vii) IMMEDIATE SOURCE:
372 (A) LIBRARY: Bovine genous
373 (B) CLONE: Lambda 9800-10
374
375 (viii) POSITION IN GENOME:
376 (C) UNITS: bp
377
378 (ix) FEATURE:
379 (A) NAME/KEY: exon
380 (B) LOCATION: 20..99
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382 (ix) FEATURE:
383 (A) NAME/KEY: intron
384 (B) LOCATION: 1..19
385
386 (ix) FEATURE:
387 (A) NAME/KEY: intron
388 (B) LOCATION: 100..119
389
390 (ix) FEATURE:
391 (A) NAME/KEY: CDS
392 (B) LOCATION: 22..99
393
394
395 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:
396
397 CCCTTGCGTG TCCCCGCAGA C GAC GTC CAC GGC TCC CAC GGC CGG CAG GTG 51
398 Asp Val His Gly Ser His Gly Arg Gln Val
399 1 5 10
400
401 TGC CGT CGG CAC GAG CTG TAC GTG AGC TTC CAG GAC CTG GGC TGG CTG 99
402 Cys Arg Arg His Glu Leu Tyr Val Ser Phe Gln Asp Leu Gly Trp Leu
403 15 20 25
404
405 GTGAGTTCCG ACTCTCCTTT 119
406
407
408 (2) INFORMATION FOR SEQ ID NO:12:
409
410 (i) SEQUENCE CHARACTERISTICS:
411 (A) LENGTH: 26 amino acids
412 (B) TYPE: amino acid
413 (D) TOPOLOGY: linear
414
415 (ii) MOLECULE TYPE: protein
416

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417 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

418
419 Asp Val His Gly Ser His Gly Arg Gln Val Cys Arg Arg His Glu Leu
420 1 5 10 15421
422 Tyr Val Ser Phe Gln Asp Leu Gly Trp Leu
423 20 25424
425 (2) INFORMATION FOR SEQ ID NO:13:426
427 (i) SEQUENCE CHARACTERISTICS:

428 (A) LENGTH: 1003 base pairs

429 (B) TYPE: nucleic acid

430 (C) STRANDEDNESS: double

431 (D) TOPOLOGY: circular

432

433 (ii) MOLECULE TYPE: cDNA to mRNA

434

435 (iii) HYPOTHETICAL: NO

436

437 (vi) ORIGINAL SOURCE:

438 (A) ORGANISM: Homo sapiens

439 (F) TISSUE TYPE: Human Heart

440

441 (vii) IMMEDIATE SOURCE:

442 (A) LIBRARY: Human heart cDNA library stratagene catalog

443 #936208

444 (B) CLONE: hh38

445

446 (viii) POSITION IN GENOME:

447 (C) UNITS: bp

448

449 (ix) FEATURE:

450 (A) NAME/KEY: CDS

451 (B) LOCATION: 8..850

452

453 (ix) FEATURE:

454 (A) NAME/KEY: mat_peptide

455 (B) LOCATION: 427..843

456

457 (ix) FEATURE:

458 (A) NAME/KEY: mRNA

459 (B) LOCATION: 1..997

460

461

462 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

463

464 GAATTCC GAG CCC CAT TGG AAG GAG TTC CGC TTT GAC CTG ACC CAG ATC 49

465 Glu Pro His Trp Lys Glu Phe Arg Phe Asp Leu Thr Gln Ile

466 -139 -135 -130

467

468 CCG GCT GGG GAG GCG GTC ACA GCT GCG GAG TTC CGG ATT TAC AAG GTG 97

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469	Pro	Ala	Gly	Glu	Ala	Val	Thr	Ala	Ala	Glu	Phe	Arg	Ile	Tyr	Lys	Val	
470	-125					-120					-115					-110	
471																	
472	CCC	AGC	ATC	CAC	CTG	CTC	AAC	AGG	ACC	CTC	CAC	GTC	AGC	ATG	TTC	CAG	145
473	Pro	Ser	Ile	His	Leu	Leu	Asn	Arg	Thr	Leu	His	Val	Ser	Met	Phe	Gln	
474					-105					-100						-95	
475																	
476	GTG	GTC	CAG	GAG	CAG	TCC	AAC	AGG	GAG	TCT	GAC	TTG	TTC	TTT	TTG	GAT	193
477	Val	Val	Gln	Glu	Gln	Ser	Asn	Arg	Glu	Ser	Asp	Leu	Phe	Phe	Leu	Asp	
478				-90					-85						-80		
479																	
480	CTT	CAG	ACG	CTC	CGA	GCT	GGA	GAC	GAG	GGC	TGG	CTG	GTG	CTG	GAT	GTC	241
481	Leu	Gln	Thr	Leu	Arg	Ala	Gly	Asp	Glu	Gly	Trp	Leu	Val	Leu	Asp	Val	
482				-75				-70						-65			
483																	
484	ACA	GCA	GCC	AGT	GAC	TGC	TGG	TTG	CTG	AAG	CGT	CAC	AAG	GAC	CTG	GGA	289
485	Thr	Ala	Ala	Ser	Asp	Cys	Trp	Leu	Leu	Lys	Arg	His	Lys	Asp	Leu	Gly	
486		-60					-55				-50						
487																	
488	CTC	CGC	CTC	TAT	GTG	GAG	ACT	GAG	GAT	GGG	CAC	AGC	GTG	GAT	CCT	GGC	337
489	Leu	Arg	Leu	Tyr	Val	Glu	Thr	Glu	Asp	Gly	His	Ser	Val	Asp	Pro	Gly	
490	-45					-40				-35						-30	
491																	
492	CTG	GCC	GGC	CTG	CTG	GGT	CAA	CGG	GCC	CCA	CGC	TCC	CAA	CAG	CCT	TTC	385
493	Leu	Ala	Gly	Leu	Leu	Gly	Gln	Arg	Ala	Pro	Arg	Ser	Gln	Gln	Pro	Phe	
494				-25					-20					-15			
495																	
496	GTG	GTC	ACT	TTC	TTC	AGG	GCC	AGT	CCG	AGT	CCC	ATC	CGC	ACC	CCT	CGG	433
497	Val	Val	Thr	Phe	Arg	Ala	Ser	Pro	Ser	Pro	Ile	Arg	Thr	Pro	Arg		
498				-10				-5						1			
499																	
500	GCA	GTG	AGG	CCA	CTG	AGG	AGG	AGG	CAG	CCG	AAG	AAA	AGC	AAC	GAG	CTG	481
501	Ala	Val	Arg	Pro	Leu	Arg	Arg	Arg	Gln	Pro	Lys	Lys	Ser	Asn	Glu	Leu	
502		5					10					15					
503																	
504	CCG	CAG	GCC	AAC	CGA	CTC	CCA	GGG	ATC	TTT	GAT	GAC	GTC	CAC	GGC	TCC	529
505	Pro	Gln	Ala	Asn	Arg	Leu	Pro	Gly	Ile	Phe	Asp	Asp	Val	His	Gly	Ser	
506	20					25					30					35	
507																	
508	CAC	GGC	CGG	CAG	GTC	TGC	CGT	CGG	CAC	GAG	CTC	TAC	GTC	AGC	TTC	CAG	577
509	His	Gly	Arg	Gln	Val	Cys	Arg	Arg	His	Glu	Leu	Tyr	Val	Ser	Phe	Gln	
510					40					45					50		
511																	
512	GAC	CTT	GGC	TGG	CTG	GAC	TGG	GTC	ATC	GCC	CCC	CAA	GGC	TAC	TCA	GCC	625
513	Asp	Leu	Gly	Trp	Leu	Asp	Trp	Val	Ile	Ala	Pro	Gln	Gly	Tyr	Ser	Ala	
514				55					60					65			
515																	
516	TAT	TAC	TGT	GAG	GGG	GAG	TGC	TCC	TTC	CCG	CTG	GAC	TCC	TGC	ATG	AAC	673
517	Tyr	Tyr	Cys	Glu	Gly	Glu	Cys	Ser	Phe	Pro	Leu	Asp	Ser	Cys	Met	Asn	
518				70				75						80			
519																	
520	GCC	ACC	AAC	CAC	GCC	ATC	CTG	CAG	TCC	CTG	GTG	CAC	CTG	ATG	AAG	CCA	721

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521 Ala Thr Asn His Ala Ile Leu Gln Ser Leu Val His Leu Met Lys Pro
522      85                      90                      95
523
524 AAC GCA GTC CCC AAG GCG TGC TGT GCA CCC ACC AAG CTG AGC GCC ACC      769
525 Asn Ala Val Pro Lys Ala Cys Cys Ala Pro Thr Lys Leu Ser Ala Thr
526 100                      105                      110                      115
527
528 TCT GTG CTC TAC TAT GAC AGC AGC AAC AAC GTC ATC CTG CGC AAG CAC      817
529 Ser Val Leu Tyr Tyr Asp Ser Ser Asn Asn Val Ile Leu Arg Lys His
530      120                      125                      130
531
532 CGC AAC ATG GTG GTC AAG GCC TGC GGC TGC CAC TGAGTCAGCC CGCCCAGCCC      870
533 Arg Asn Met Val Val Lys Ala Cys Gly Cys His
534      135                      140
535
536 TACTGCAGCC ACCCTTCTCA TCTGGATCGG GCCCTGCAGA GGCAGAAAAC CCTTAAATGC      930
537
538 TGTCACAGCT CAAGCAGGAG TGTCAGGGGC CCTCACTCTC GGTGCCTACT TCCTGTCAGG      990
539
540 CTTCTGGGAA TTC      1003
541
542
543 (2) INFORMATION FOR SEQ ID NO:14:
544
545 (i) SEQUENCE CHARACTERISTICS:
546 (A) LENGTH: 281 amino acids
547 (B) TYPE: amino acid
548 (D) TOPOLOGY: linear
549
550 (ii) MOLECULE TYPE: protein
551
552 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:
553
554 Glu Pro His Trp Lys Glu Phe Arg Phe Asp Leu Thr Gln Ile Pro Ala
555 -139                      -135                      -130                      -125
556
557 Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile Tyr Lys Val Pro Ser
558      -120                      -115                      -110
559
560 Ile His Leu Leu Asn Arg Thr Leu His Val Ser Met Phe Gln Val Val
561      -105                      -100                      -95
562
563 Gln Glu Gln Ser Asn Arg Glu Ser Asp Leu Phe Phe Leu Asp Leu Gln
564      -90                      -85                      -80
565
566 Thr Leu Arg Ala Gly Asp Glu Gly Trp Leu Val Leu Asp Val Thr Ala
567 -75                      -70                      -65                      -60
568
569 Ala Ser Asp Cys Trp Leu Leu Lys Arg His Lys Asp Leu Gly Leu Arg
570      -55                      -50                      -45
571
572 Leu Tyr Val Glu Thr Glu Asp Gly His Ser Val Asp Pro Gly Leu Ala

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573          -40          -35          -30
574
575 Gly Leu Leu Gly Gln Arg Ala Pro Arg Ser Gln Gln Pro Phe Val Val
576          -25          -20          -15
577
578 Thr Phe Phe Arg Ala Ser Pro Ser Pro Ile Arg Thr Pro Arg Ala Val
579          -10          -5          1          5
580
581 Arg Pro Leu Arg Arg Arg Gln Pro Lys Lys Ser Asn Glu Leu Pro Gln
582          10          15          20
583
584 Ala Asn Arg Leu Pro Gly Ile Phe Asp Asp Val His Gly Ser His Gly
585          25          30          35
586
587 Arg Gln Val Cys Arg Arg His Glu Leu Tyr Val Ser Phe Gln Asp Leu
588          40          45          50
589
590 Gly Trp Leu Asp Trp Val Ile Ala Pro Gln Gly Tyr Ser Ala Tyr Tyr
591          55          60          65
592
593 Cys Glu Gly Glu Cys Ser Phe Pro Leu Asp Ser Cys Met Asn Ala Thr
594          70          75          80          85
595
596 Asn His Ala Ile Leu Gln Ser Leu Val His Leu Met Lys Pro Asn Ala
597          90          95          100
598
599 Val Pro Lys Ala Cys Cys Ala Pro Thr Lys Leu Ser Ala Thr Ser Val
600          105          110          115
601
602 Leu Tyr Tyr Asp Ser Ser Asn Asn Val Ile Leu Arg Lys His Arg Asn
603          120          125          130
604
605 Met Val Val Lys Ala Cys Gly Cys His
606          135          140

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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/07/800,364A

DATE: 01/04/93
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LINE ERROR

ORIGINAL TEXT

27 Wrong application Serial Number
443 Response Exceeds Line Limitations

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1

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S3925

MANDATORY IDENTIFIER THAT WAS NOT FOUND

PRIOR APPLICATION DATA
APPLICATION NUMBER
FILING DATE

PAGE: 1

SEQUENCE CORRECTION REPORT
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DATE: 01/04/93
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S3925

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CORRECTED TEXT